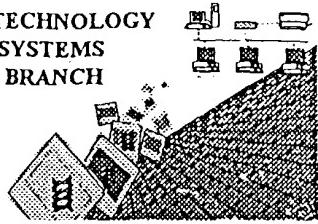


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/720,840  
Source: IFW0 -  
Date Processed by STIC: 4/23/04 -

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/920,840</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. <b>Do not use tab codes between numbers; use space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was <b>not</b> saved in ASCII(DOS) text, as required by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input checked="" type="checkbox"/> Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



IF

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/720,840

DATE: 04/23/2004

TIME: 10:32:40

Input Set : A:\pto.da.txt  
 Output Set: N:\CRF4\04232004\J720840.raw

3 <110> APPLICANT: Schwartz, David A.  
 4 Hogrefe, Richard I.  
 6 <120> TITLE OF INVENTION: FUNCTIONAL BIOPOLYMER MODIFICATION  
 7 REAGENTS AND USES THEREOF  
 9 <130> FILE REFERENCE: 37154-751  
 -> 11 <140> CURRENT APPLICATION NUMBER: US/10/720,840  
 -> 12 <141> CURRENT FILING DATE: 2003-11-24  
 14 <160> NUMBER OF SEQ ID NOS: 5  
 16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## STORED SEQUENCES

69 <210> SEQ ID NO: 5  
 70 <211> LENGTH: 18  
 71 <212> TYPE: DNA  
 72 <213> ORGANISM: Artificial Sequence  
 74 <220> FEATURE:  
 75 <223> OTHER INFORMATION: Synthetic oligonucleotide  
 77 <400> SEQUENCE: 5  
 78 cctaacctgt cctaaagtt 18  
 -> 80 (1) *delete*

(see p. 2)

*Does Not Comply  
Corrected Diskette Needed*

10/720,840

2

<210> 2  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> 1  
<223> n = 6-(4-formylbenzoylamino)hexyl phosphodiester

<223> Synthetic aldehyde amidite-oligonucleotide conjugate

<400> 2  
n tttttttag ccttaactgat gccatg

<210> 3  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222>  
<223> fluorescein bound at 5' end to form fluorescein-oligonucleotide conjugate

<223> Synthetic fluorescein-oligonucleotide conjugate

<400> 3  
n catggcatac agttacgct

26

19

← "n" can only represent a single nucleotide.  
(See item 13 on Error Summary Sheet)

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/720,840

DATE: 04/23/2004  
TIME: 10:32:41

Input Set : A:\pto.da.txt  
Output Set: N:\CRF4\04232004\J720840.raw

11 M:270 C: Current Application Number differs, Replaced Current Application Number  
12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
12 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
13 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
57 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
30 M:254 E: No. of Bases conflict, this line has no nucleotides.